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07 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
10 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
13 61 HGLLRKRLVCGTGHGHLPPGSGVGTTRQHSFLGFLFISAVGVGVSIRGVSGSLYL 120
16 61 HGLLRKRLVCGTGHGHLPPGSGVGTTRQHSFLGFLFISAVGVGVSIRGVSGSLYL 120
19 121 MNRGELVGGSKITSPFTRPGVTFVAVNYVSSNLYKHDLGKRYVALNKGTPROGAR 180
22 121 MNRGELVGGSKITSPFTRPGVTFVAVNYVSSNLYKHDLGKRYVALNKGTPROGAR 180
25 181 SKRHKTFHFLPRVDPPEVPELYKDLMT 211
28 181 SKRHKTFHFLPRVDPPEVPELYKDLMT 211

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RESULT 2

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07 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
10 01-MAR-2001 (Tremblrel. 16, created)
13 01-MAR-2001 (Tremblrel. 15, last sequence update)
16 01-MAR-2001 (Tremblrel. 16, last annotation update)
19 FGF-20.
22 Rattus norvegicus (Rat).
25 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
28 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
31 NCBI_TaxID: 10116;
34 SEQUENCE FROM N.A.
37 Pubmed: 11032730;
40 Tissue: Aorta, brain.
43 Genbank: AF040217; BAH176311;
46 Sequence: 212 AA; 23537 MW; 4785866FL7728977 CIRC64;

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Query Match 96.1%; Score 1074; FR 11; Length 212;
 Best Local Similarity 95.3%; Pred. No. 3, 96-94;
 Matches 209; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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07 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
10 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
13 61 HGLLRKRLVCGTGHGHLPPGSGVGTTRQHSFLGFLFISAVGVGVSIRGVSGSLYL 120
16 61 HGLLRKRLVCGTGHGHLPPGSGVGTTRQHSFLGFLFISAVGVGVSIRGVSGSLYL 120
19 121 MNRGELVGGSKITSPFTRPGVTFVAVNYVSSNLYKHDLGKRYVALNKGTPROGAR 180
22 121 MNRGELVGGSKITSPFTRPGVTFVAVNYVSSNLYKHDLGKRYVALNKGTPROGAR 180
25 181 SKRHKTFHFLPRVDPPEVPELYKDLMT 211
28 181 SKRHKTFHFLPRVDPPEVPELYKDLMT 211

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07 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
10 01-MAR-2001 (Tremblrel. 16, created)
13 01-MAR-2001 (Tremblrel. 16, last sequence update)
16 01-MAR-2001 (Tremblrel. 16, last annotation update)
19 FGF-20.
22 Rattus norvegicus (Rat).
25 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
28 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
31 NCBI_TaxID: 10116;
34 SEQUENCE FROM N.A.
37 Pubmed: 11032730;
40 Tissue: Aorta, brain.
43 Genbank: AF040217; BAH176311;
46 Sequence: 212 AA; 23537 MW; 4785866FL7728977 CIRC64;

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08 Mus musculus (Mouse).
11 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
14 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
17 NCBI_TaxID: 10090;
20 SEQUENCE FROM N.A.
23 Pubmed: 1041498;
26 Submitted (SPR-2000) to the EMBL/GenBank/DDBJ databases.
29 EMBL: AB049218; BAB16406;
32 Sequence: 212 AA; 23659 MW; 1741828915B696F CIRC64;

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Query Match 95.6%; Score 1069; FR 11; Length 212;
 Best Local Similarity 94.8%; Pred. No. 1, 20-93;
 Matches 209; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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07 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
10 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
13 61 HGLLRKRLVCGTGHGHLPPGSGVGTTRQHSFLGFLFISAVGVGVSIRGVSGSLYL 120
16 61 HGLLRKRLVCGTGHGHLPPGSGVGTTRQHSFLGFLFISAVGVGVSIRGVSGSLYL 120
19 121 MNRGELVGGSKITSPFTRPGVTFVAVNYVSSNLYKHDLGKRYVALNKGTPROGAR 180
22 121 MNRGELVGGSKITSPFTRPGVTFVAVNYVSSNLYKHDLGKRYVALNKGTPROGAR 180
25 181 SKRHKTFHFLPRVDPPEVPELYKDLMT 211
28 181 SKRHKTFHFLPRVDPPEVPELYKDLMT 211

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RESULT 4

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07 1 MAPLAEVGGFLGGLEGGVGGSHFLPPAGGERPPLIGERRSAERSARGGGGAQIAHL 60
10 01-MAY-2000 (Tremblrel. 13, created)
13 01-MAY-2000 (Tremblrel. 13, last sequence update)
16 01-MAY-2000 (Tremblrel. 16, last annotation update)
19 XFGF-20.
22 Xenopus laevis (African clawed frog).
25 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
28 Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
31 NCBI_TaxID: 6355;
34 SEQUENCE FROM N.A.
37 Medline: 9973151; Pubmed: 1041498;
40 Koga G., Adachi N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,
43 Terai H., Sakaki Y., Kurokawa T., Yoshizawa K., K.
46 "Characterization of a novel member of the FGF family, XFGF-20, in
49 the frog, Xenopus laevis."
52 Biochem. Biophys. Res. Commun. 261:756-765 (1999).
55 EMBL: AB012615; BAAB3474.1;
58 HSP: P05230; ZABG.
61 Interpro: IPR002299;
64 Pfam: PF00167; FGF;
67 PRINTS: PR00263; HGF;
70 PROSITE: PS00247; HGF_FGF;
73 SMART: SM00442; FGF;
76 Sequence: 208 AA; 23438 MW; 268881634570430 CIRC64.

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Query Match 80.9%; Score 904.5; FR 13; Length 208;
 Best Local Similarity 80.6%; Pred. No. 4, 66-78;
 Matches 170; Conservative 19; Mismatches 19; Indels 3; Gaps 2;


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10 01 OCT 2000 (FEBRUARY 15, last sequence update)
11 01 MAR 2001 (FEBRUARY 15, last annotation update)
12 PROBABLY GROWTH FACTOR HOMEODOMAIN FACTOR 4 (HGF4) 18
13 HGF-4
14 GALLUS GALLUS (Chickens)
15 Eukaryotic Molecular Cloning: Vertebrate Eukaryotic
16 Archaeosaurus Aves: Neofunctional (allotopes), Plastidial, Plastidial
17 GALLUS
18 NBI_TaxID: 9031
19
20 SEQUENCE FROM N.A.
21 MEDLINE: 20112624; PubMed: 1044716
22 Kamez-Shanjan L, Smallwood PM, Nathans J
23 "Structural diversity of the Eukaryotic Growth Homeodomain Factors
24 is associated by Alternative Promoter Usage and Differential
25 Splicing."
26 J Biol Chem 275:2557-2563 (2000)
27
28 EMBL: AF199606; AAF31393.1
29 GenBank: U0002309
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31 GenBank: U0002309
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33 GenBank: U0002309
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101 01 OCT 2000 (FEBRUARY 15, last sequence update)
102 01 MAR 2001 (FEBRUARY 15, last annotation update)
103 PROBABLY GROWTH FACTOR HOMEODOMAIN FACTOR 4 (HGF4) 18
104 HGF-4
105 GALLUS GALLUS (Chickens)
106 Eukaryotic Molecular Cloning: Vertebrate Eukaryotic
107 Archaeosaurus Aves: Neofunctional (allotopes), Plastidial, Plastidial
108 GALLUS
109 NBI_TaxID: 9031
110
111 SEQUENCE FROM N.A.
112 MEDLINE: 20112624; PubMed: 1044716
113 Kamez-Shanjan L, Smallwood PM, Nathans J
114 "Structural diversity of the Eukaryotic Growth Homeodomain Factors
115 is associated by Alternative Promoter Usage and Differential
116 Splicing."
117 J Biol Chem 275:2557-2563 (2000)
118 EMBL: AF199606; AAF31393.1
119 GenBank: U0002309
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